

primus

201	WVLTAAHCKK PNLQV....F LGKHNLRQRE SSQEQQSSVVR AVIHPDY... WVVTAAHCKK PKYTV....R LGDHSLQNKD GPEQEIPVVQ SIPHPCY... WVVSAGHCYK SRIQV....R LGEHNIEVLE GNEQFINAAK IIRHPQY... WVLTAAHCKM NEYTV....H LGSDTLGDRR A..QRIKASK SFRHPGY... WVLTAAHCFP ERNRVLSRWR VFAGAVAQAS PHGLQLGVQA VVYHGGYLPF	250	SEQ ID No. 1 SEQ ID No. 2 SEQ ID No. 3 SEQ ID No. 4 SEQ ID No. 5
Prom	...DAASHDQ	251	DIMLLRLARP AKLSELIQPL PLERDCSA.. NTTSCHILGW
Tadg14	NSSDVEDHMH	DLMILLQLRDQ ASLGSKVKPI SLADHCTQ.. PGQNCTVSGW	
Try1	...DRKTLNN	DIMLILKLSSR AVINARVSTI SLPTAPP.. TGTKCLISGW	
Scce	ST...QTHVN	DLMLVKLNSQ ARLSSMVKKV RLPSRCEP.. PGTTCTVSGW	
Heps	RDPNSEENSN	DIALVHLSSP LPLTEYIQPV CLPAAGQALV DGKICTVTGW	
301	GKTAD..GDF PDTIQCAYIH LVSREECEHA ..YPGQITQN MLCAGDEKYG GTVTSPRENF PDTLNCAEVK IFPKKKCEDA ..YPGQITDG MVCAGSSK.G GNTASSGADY PDELQCLDAP VLSQAKCEAS ..YPGKITSN MFCVGFLEGG GTTTSPDVTF PSDLMCVDVK LISPDQDKV ..YKDLLENS MLCAGIPDSK GNTQYYGQQ. AGVLQEARVP IISNDVCNGA DFYGNQIKPK MFCAGYPEGG	350	
Prom	KDSCCGDSSG	351	SEQ ID No. 1
Tadg14	ADTCGGDSSG	SEQ ID No. 2	
Try1	KDSCCGDSSG	SEQ ID No. 3	
Scce	KNACNGDSSG	SEQ ID No. 4	
Heps	IDACCGDSSG	SEQ ID No. 5	

Figure 2. Comparison of amino acid sequence of TADG-14 with known serine protease catalytic domains.

1027 CAGAACAAAGTGTGAGAGAGCCTATCCAGGAAGATCACCGAGGGCATGGT 1076
1056 CAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACAGATGGCATGGT 1105

1077 CTGTGCTGGCAGCAGCAATGGAGCTGACACGTGCCAGGGTGACTCAGGAG 1126
1106 CTGTGCAGGCAGCAGCAAAGGGCTGACACGTGCCAGGGCGATTCTGGAG 1155

1127 GCCCTCTGGTGTGCCACGGGATGCTCCAGGGCATCACCTCATGGGCTCA 1176
1156 GCCCCCTGGTGTGTGATGGTGCACTCCAGGGCATCACATCCTGGGCTCA 1205

1177 GACCCCTGTGGAAACCCGAGAAACCTGGAGTCTACACCAAAATCTGCCG 1226
1206 GACCCCTGTGGAGGTCCGACAAACCTGGCGTCTATACCAACATCTGCCG 1255

1227 CTACACTACCTGGATCAAGAAGACCATGGACAACAGGGACTGATCCTGG 1275 SEQ ID No. 8
1256 CTACCTGGACTGGATCAAGAAGATCATAGGCAGCAAGGGCTGATTCTAG 1304 SEQ ID No. 9

Percent Similarity: 77.220 Percent Identity: 72.201

Match display thresholds for the alignment(s):

IDENTITY

2

T14pro.Jack x Neur.Jack May 8, 1997 09:27 ..

Tadg14 1 MGRPRPRAAKTWMFLGGAWAGHSRAQEDKVLGGHECOPHSQPWQAAL 50

Neurop 1 MGRPPPCAIOPWILLLLFMGAAGLTRAQSKILEGRECIPHSQPWOAAL 50

51 FOGOOLLCGGVLVGGNWVLAAHCKKPKYTVRLGDHSQNKGPEQEIPV 100

5.1 EOGERLJICGGVLTGDRWYLTAAHCKKOKYSVRLGDHSLOSRDOPEOEIOV 100

101 VOSIPHPCYNSSDVEDHNHDLMLLORDOASLGSKVKPISLADHCTOPGQ 150

VQSTIFAFCTINSSDVEEDHNADLMLQEQRDQASSEGRVRIISLADKOTLG

101 AOSTOHP CYNNSNPEDHSHDIMI TBLONSANLGDKVKPVOLANLCPKVGO 150

151 KCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQITDGMVCAG 200

RCTIVSGWGIVISPRENFPDIENCAEVKTFYQKCELBATTCGQFISBENVQD
|| : || || || || || || : || || || || || : ||

161 KCLISCGWCTVTSPQENERTNLNCAEVKLYSONKCERAYPGKLTGGMVCA 200

201 SSKGADTCOGDGGPLVCDGALOGITSWGSDPCGRSDKPGVYTNICRYLD 250

SSRGADTCQGDSGGPLVCDGALQGTISWGSDPCGRSDRFGVITINICRTE

201 SSNCADTCGCGCGCIVCGCGMIGITSWGSDPGKPEKPGVYTKICRYTT 250

251 WIKKIIGOG 260 SEQ TO No. 7

WIRKIIIGSKG 260 SEQ. NO. 1
|||||

251. УЧИТЕЛЬСТВО В СССР. 680 ТД № 10

Figure 8. Amino acid homolog.

Figure 8. Amino acid homology of TADG-14 with mouse neuropsin.



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANT: O'Brien, et al. § ART UNIT:
§ 1814
FILED: August 21, 1997 §
§ EXAMINER:
SERIAL NO.: 08/915,659 § Jacobson, D.
§
FOR: Novel Extracellular Serine §
Protease § DOCKET: D6020

The Assistant Commissioner of Patents and Trademarks
BOX MISSING PARTS
Washington, DC 20231

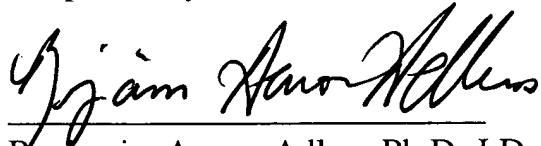
**COMPLIANCE OF REQUIREMENTS FOR PATENT APPLICATIONS
CONTAINING NUCLEOTIDE AND/OR AMINO ACID SEQUENCE
DISCLOSURES**

Dear Sir:

Applicant provides a computer readable form of the Sequence Listing on the enclosed 3.5 inch disk and a paper copy thereof for the above-referenced application. The disk is 1.44 Mb Macintosh-formatted disk. The file is stored as D6020SEQ in text format. I hereby state that the content of the paper copy of the Sequence Listing filed as part of the above-captioned application and the enclosed computer readable copy of the Sequence Listing are the same.

Respectfully submitted,

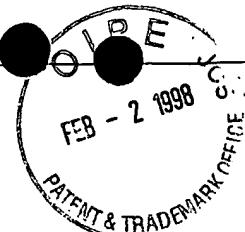
Date: Jan. 28, 1998



Benjamin Aaron Adler, Ph.D.,J.D.

Counsel for Applicant
Registration No. 35,423

McGREGOR & ADLER, P.C.
8011 Candle Lane
Houston, Texas 77071
(713) 777-2321



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: O'Brien et al
- (ii) TITLE OF INVENTION: Novel Extracellular Serine Protease
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
 - (B) STREET: 8011 Candle Lane
 - (C) CITY: Houston
 - (D) STATE: Texas
 - (E) ZIP: 77071
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: 1.44 Mb floppy disk
 - (B) COMPUTER: Apple Macintosh
 - (C) OPERATING SYSTEM: Macintosh
 - (D) SOFTWARE: Microsoft Word for Macintosh
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/915,659
 - (B) FILING DATE: August 21, 1997
 - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATE:
 - (A) APPLICATION NUMBER: /
 - (B) FILING DATE: /
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Benjamin Aaron Adler, Ph.D.
 - (B) REGISTRATION NUMBER: 35,423
 - (C) REFERENCE/DOCKET NUMBER: D6020
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (713) 777-2321

(B) TELEFAX: (713) 777-6908

(2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: protein
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLIC INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 1

Trp Val Leu Thr Ala Ala His Cys Lys Lys Pro Asn Leu Gln Val
5 10 15

Phe Leu Glu Lys His Asn Leu Arg Gln Arg Glu Ser Ser Gln Glu
20 25 30

Gln Ser Ser Val Val Arg Ala Val Ile His Pro Asp Tyr Asp Ala
35 40 45

Ala Ser His Asp Gln Asp Ile Met Leu Leu Arg Leu Ala Arg Pro
50 55 60

Ala Lys Leu Ser Glu Leu Ile Gln Pro Leu Pro Leu Glu Arg Asp
65 70 75

Cys Ser Ala Asn Thr Thr Ser Cys His Ile Leu Gly Trp Gly Lys
80 85 90

Thr Ala Asp Gly Asp Phe Pro Asp Thr Ile Gln Cys Ala Tyr Ile
95 100 105

His Leu Val Ser Arg Glu Glu Cys Glu His Ala Tyr Pro Gly Gln
110 115 120

Ile Thr Gln Asn Met Leu Cys Ala Gln Asp Glu Lys Tyr Gly Lys
125 130 135

Asp Ser Cys Gln Gly Asp Ser Gly Gly
140

(3) INFORMATION FOR SEQ ID NO: 2

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: protein
- (iii) HYPOTHETICAL: no
- (iv) ANTISENSE: no
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (vii) IMMEDIATE SOURCE:
- (viii) POSITION IN GENOME:
- (ix) FEATURE:
- (x) PUBLICATION INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 2

Trp Val Val Thr Ala Ala His Cys Lys Lys Pro Lys Tyr Thr Val
5 10 15

Arg Leu Gly Asp His Ser Leu Gln Asn Lys Asp Gly Pro Glu Gln
20 25 30

Glu Ile Pro Val Val Gln Ser Ile Pro His Pro Cys Tyr Asn Ser
35 40 45

Ser Asp Val Glu Asp His Asn His Asp Leu Met Leu Leu Gln Leu
50 55 60

Arg Asp Gln Ala Ser Leu Gly Ser Lys Val Lys Pro Ile Ser Leu
65 70 75

Ala Asp His Cys Thr Gln Pro Gly Gln Asn Cys Thr Val Ser Gly
80 85 90

Trp Gly Thr Val Thr Ser Pro Arg Glu Asn Phe Pro Asp Thr Leu
95 100 105

Asn Cys Ala Glu Val Lys Ile Phe Pro Gln Lys Lys Cys Glu Asp
110 115 120

Ala Tyr Pro Gly Gln Ile Thr Asp Gly Met Val Cys Ala Gly Ser
125 130 135

Ser Lys Gly Ala Asp Thr Cys Gln Gly Asp Ser Gly Gly
140 145

(4) INFORMATION FOR SEQ ID NO: 3

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: protein
- (iii) HYPOTHETICAL: no
- (iv) ANTISENSE: no
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (vii) IMMEDIATE SOURCE:
- (viii) POSITION IN GENOME:
- (ix) FEATURE:
- (x) PUBLICATION INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 3

Trp Val Val Ser Ala Gly His Cys Tyr Lys Ser Arg Ile Gln Val
5 10 15

Arg Leu Gly Glu His Asn Ile Glu Val Leu Glu Gly Asn Glu Gln
20 25 30

Phe Ile Asn Ala Ala Lys Ile Ile Arg His Pro Gln Tyr Asp Arg
35 40 45

Lys Thr Leu Asn Asn Asp Ile Met Leu Ile Lys Leu Ser Ser Arg
50 55 60

Ala Val Ile Asn Ala Arg Val Ser Thr Ile Ser Leu Pro Thr Ala
65 70 75

Pro Pro Ala Thr Gly Thr Lys Cys Leu Ile Ser Gly Trp Gly Asn
80 85 90

Thr Ala Ser Ser Gly Ala Asp Tyr Pro Asp Glu Leu Gln Cys Leu
95 100 105

Asp Ala Pro Val Leu Ser Gln Ala Lys Cys Glu Ala Ser Tyr Pro
110 115 120

Gly Lys Ile Thr Ser Asn Met Phe Cys Val Gly Phe Leu Glu Gly
125 130 135

Gly Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly
140 145

(5) INFORMATION FOR SEQ ID NO: 4

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: protein
- (iii) HYPOTHETICAL: no
- (iv) ANTISENSE: no
- (v) FRAGMENT TYPE: internal
- (vi) ORIGINAL SOURCE:
- (vii) IMMEDIATE SOURCE:
- (viii) POSITION IN GENOME:
- (ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 4

Trp Val Leu Thr Ala Ala His Cys Lys Met Asn Glu Tyr Thr Val
5 10 15

His Leu Gly Ser Asp Thr Leu Gly Asp Arg Arg Ala Gln Arg Ile
20 25 30

Lys Ala Ser Lys Ser Phe Arg His Pro Gly Tyr Ser Thr Gln Thr
35 40 45

His Val Asn Asp Leu Met Leu Val Lys Leu Asn Ser Gln Ala Arg
50 55 60

Leu Ser Ser Met Val Lys Lys Val Arg Leu Pro Ser Arg Cys Glu
65 70 75

Pro Pro Gly Thr Thr Cys Thr Val Ser Gly Trp Gly Thr Thr Thr
80 85 90

Ser Pro Asp Val Thr Phe Pro Ser Asp Leu Met Cys Val Asp Val
95 100 105

Lys Leu Ile Ser Pro Gln Asp Cys Thr Lys Val Tyr Lys Asp Leu
110 115 120

Leu Glu Asn Ser Met Leu Cys Ala Gly Ile Pro Asp Ser Lys Lys
125 130 135

Asn Ala Cys Asn Gly Asp Ser Gly Gly
140

(6) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: protein

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:
(vii) IMMEDIATE SOURCE:
(viii) POSITION IN GENOME:
(ix) FEATURE:
(x) PUBLICATION INFORMATION:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 5

Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg Asn Arg Val
5 10 15

Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln Ala Ser
20 25 30

Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His Gly
35 40 45

Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser Asn
50 55 60

Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Glu
65 70 75

Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Val
80 85 90

Asp Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Tyr
95 100 105

Tyr Gly Gln Gln Ala Gly Val Leu Gln Glu Ala Arg Val Pro Ile
110 115 120

Ile Ser Asn Asp Val Cys Asn Gly Ala Asp Phe Tyr Gly Asn Gln
125 130 135

Ile Lys Pro Lys Met Phe Cys Ala Gly Tyr Pro Glu Gly Gly Ile
140 145 150

Asp Ala Cys Gln Gly Asp Ser Gly Gly
155

(7) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1343 bp
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single-stranded

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

(A) DESCRIPTION: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 6

CTGTAGCAGG	CAGAGCTTAC	CAAGTCTCTC	CGAACTCAA	TGGAAGAAAT	ACCTTATGAA	60
TGTAAGAATG	TAGGGGGTCA	TGGCTTGTAA	TTTACACAGT	GTAAATGAAA	CCATCCTAGA	120
GGATTATGAG	GAATCCTTTC	TATGTGATTT	TCAATCATAG	CAAGCAAGAA	AGGCTCCAGT	180
GTCAAGGTAG	TTCAGCTCTT	ACAGGATATA	AAACAGTCCA	TACTTGAGAG	AAAAAACTTA	240
GATCTGAGTG	ATGGAATGTG	AAGCAAATCT	TTCAAAATCA	GTAGACATT	CTTGGACATA	300
AAACACAGAT	GAGGAAAGGG	CTTCAAATTAA	GAAGTTACGT	AATCACCATC	AGAAAGTTCA	360
TGTTTGGTAA	ATTCTGTTAC	TAGAAATGTA	GGAAATTCA	GTATAGCTT	GAATCCCAAT	420
TACACATTGG	TCAGTGGAA	AACTAAGGGC	CTCCAACAGG	CAAATTCA	GAGGATAGGT	480
TTCAGGGAAT	GCCCTGGATT	CTGGAAGACC	TCACCATGGG	ACGCCCGA	CCTCGTGC	540
CCAAGACGTG	GATGTTCC	CTCTTGCTGG	GGGGAGCCTG	GGCAGGACAC	TCCAGGGCAC	600
AGGAGGACAA	GGTGTGCGG	GGTCATGAGT	GCCAACCCCCA	TTCGCAGCCT	TGGCAGGC	660
CCTTGTCCA	GGGCCAGCAA	CTACTCTGTG	GCAGGTGCCT	TGTAGGTGGC	AACTGGGTCC	720
TTACAGCTGC	CCACTGTA	AAACCGAAAT	ACACAGTACG	CCTGGGAGAC	CACAGCCTAC	780
AGAATAAAGA	TGGCCCAGAG	CAAGAAATAC	CTGTGGTTCA	GTCCATCCC	CACCCCTGCT	840
ACAACACGAG	CGATGTGGAG	GACCACAA	ATGATCTGAT	GCTTCTCAA	CTGCGTGACC	900
AGGCATCCCT	GGGGTCCAAA	GTGAAGCCA	TCAGCCTGGC	AGATCATTGC	ACCCAGCCTG	960
GCCAGAAGTG	CACCGTCTCA	GGCTGGGCA	CTGTCACCAG	TCCCCGAGAG	AATTTCCTG	1020
ACACTCTCAA	CTGTGCA	GTAAAAATCT	TTCCCCAGAA	GAAGTGTGAG	GATGCTTAC	1080
CGGGGCAGAT	CACAGATGGC	ATGGTCTGTG	CAGGCA	CAAAGGGCT	GACACGTGCC	1140
AGGGCGATTG	TGGAGGCC	CTGGTGTGTG	ATGGTGC	CCAGGGCATC	ACATCCTGGG	1200
GCTCAGACCC	CTGTGGGAGG	TCCGACAAAC	CTGGCGTCTA	TACCAACATC	TGCCGCTACC	1260
TGGACTGGAT	CAAGAAGATC	ATAGGCAGCA	AGGGCTGATT	CTAGGATAAG	CACTAGATCT	1320
CCCTTAATAA	ACTCACGGAA	TTC				1343

(8) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE:
(A) DESCRIPTION: protein
(iii) HYPOTHETICAL: no
(iv) ANTISENSE: no
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(vii) IMMEDIATE SOURCE:
(viii) POSITION IN GENOME:
(ix) FEATURE:
(x) PUBLICATION INFORMATION:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 7

Met Gly Arg Pro Arg Pro Arg Ala Ala Lys Thr Trp Met Phe Leu
5 10 15

Leu Leu Leu Gly Gly Ala Trp Ala Gly His Ser Arg Ala Gln Glu
20 25 30

Asp Lys Val Leu Gly Gly His Glu Cys Gln Pro His Ser Gln Pro
35 40 45

Trp Gln Ala Ala Leu Phe Gln Gly Gln Gln Leu Leu Cys Gly Gly
50 55 60

Val Leu Val Gly Gly Asn Trp Val Leu Thr Ala Ala His Cys Lys
65 70 75

Lys Pro Lys Tyr Thr Val Arg Leu Gly Asp His Ser Leu Gln Asn
80 85 90

Lys Asp Gly Pro Glu Gln Glu Ile Pro Val Val Gln Ser Ile Pro
95 100 105

His Pro Cys Tyr Asn Ser Ser Asp Val Glu Asp His Asn His Asp
110 115 120

Leu Met Leu Leu Gln Leu Arg Asp Gln Ala Ser Leu Gly Ser Lys
125 130 135

Val Lys Pro Ile Ser Leu Ala Asp His Cys Thr Gln Pro Gly Gln
140 145 150

Lys Cys Thr Val Ser Gly Trp Gly Thr Val Thr Ser Pro Arg Glu
155 160 165

Asn Phe Pro Asp Thr Leu Asn Cys Ala Glu Val Lys Ile Phe Pro
170 175 180

Gln Lys Lys Cys Glu Asp Ala Tyr Pro Gly Gln Ile Thr Asp Gly
185 190 195

Met Val Cys Als Gly Ser Ser Lys Gly Ala Asp Thr Cys Gln Gly
200 205 210

Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Ala Leu Gln Gly Ile
215 220 225

Thr Ser Trp Gly Ser Asp Pro Cys Gly Arg Ser Asp Lys Pro Gly
230 235 240

Val Tyr Thr Asn Ile Cys Arg Tyr Leu Asp Trp Ile Lys Lys Ile
245 250 255

Ile Gly Ser Lys Gly
260

(9) INFORMATION FOR SEQ ID NO: 8

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 799 bp
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single-stranded
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: other nucleic acid
- (iii) HYPOTHETICAL: no
- (iv) ANTISENSE: no
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (vii) IMMEDIATE SOURCE:
- (viii) POSITION IN GENOME:
- (ix) FEATURE:
- (x) PUBLICATION INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 8

AGAGGCCACC	ATGGGACGCC	CCCCACCCCTG	TGCAATCCAG	CCGTGGATCC	TTCTGCTTCT	60
GTTCATGGGA	GCGTGGGCAG	GGCTCACCAAG	AGCTCAGGGC	TCCAAGATCC	TGGAAGGTG	120
AGAGTGTATA	CCCCACTCCC	AGCCTTGGCA	GGCAGCCTTG	TTCCAGGGCG	AGAGACTGAT	180
CTGTGGGGGT	GTCCTGGTTG	GAGACAGATG	GGTCCTCACG	GCAGCCCAC	GCAAAAAACA	240
GAAGTACTCC	GTGCGTCTGG	GTGATCATAG	CCTCCAGAGC	AGAGATCAGC	CGGAGCAGGA	300
GATCCAGGTG	GCTCAGTCTA	TCCAGCATCC	TTGCTACAAAC	AACAGCAACC	CAGAAGATCA	360
CAGTCACGAT	ATAATGCTCA	TTCGACTGCA	GAACTCAGCA	AACCTGGGG	ACAAGGTCAA	420
GCCGGTCCAA	CTGGCCAATC	TGTGTCCCAA	AGTTGGCCAG	AAGTGCATCA	TATCAGGCTG	480
GGGCACTGTC	ACCAGCCCTC	AAGAGAACCTT	TCCAAACACC	CTCAACTGTG	CGGAAGTGAA	540
AATCTATTCC	CAGAACAAAGT	GTGAGAGAGC	CTATCCAGGG	AAGATCACCG	AGGGCATGGT	600
CTGTGCTGGC	AGCAGCAATG	GAGCTGACAC	GTGCCAGGGT	GACTCAGGAG	GCCCTCTGGT	660
GTGCGACGGG	ATGCTCCAGG	GCATCACCTC	ATGGGGCTCA	GACCCCTGTG	GGAAACCCGA	720
GAAACCTGGA	GTCTACACCA	AAATCTGCCG	CTACACTACC	TGGATCAAGA	AGACCATGGA	780
CAACAGGGAC	TGATCCTGG					799

(10) INFORMATION FOR SEQ ID NO: 9

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 bp
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single-stranded
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE:

- (A) DESCRIPTION: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTISENSE: no

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(vii) IMMEDIATE SOURCE:

(viii) POSITION IN GENOME:

(ix) FEATURE:

(x) PUBLICATION INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO.: 9

AGACCTZACC	ATGGGACGCC	CCCGACCTCG	TGCGGCCAAG	ACGTGGATGT	TCCTGCTCTT	60
GCTGGGGGGA	GCCTGGCAG	GACACTCCAG	GGCACAGGAG	GACAAGGTGC	TGGGGGGTCA	120
TGAGTGCCAA	CCCCATTGCG	AGCCTTGGCA	GGCGGCCTTG	TTCCAGGGCC	AGCAACTACT	180
CTGTGGCGGT	GTCCTTGTAG	GTGGCAACTG	GGTCCTTACA	GCTGCCACT	GTAAAAAAC	240
GAAATACACA	GTACGCCTGG	GAGACCACAG	CCTACAGAAAT	AAAGATGGCC	CAGAGCAAGA	300
AATACCTGTG	GTTCAACTGCA	TCCCACACCC	CTGCTACAAAC	AGCAGCGATG	TGGAGGACCA	360
CAACCATGAT	CTGATGCTTC	TTCAACTGCG	TGACCAGGCA	TCCCTGGGGT	CCAAAGTGAA	420

GCCCCATCAGC	CTGGCAGATC	ATTGCACCCA	GCCTGGCCAG	AAGTGCACCG	TCTCAGGCTG	480
GGGCACTGTC	ACCACTCCCC	GAGAGAATT	TCCTGACACT	CTCAACTGTG	CAGAAAGTAAA	540
AATCTTCCC	CAGAAGAAGT	GTGAGGATGC	TTACCCGGGG	CAGATCACAG	ATGGCATGGT	600
CTGTGCAGGC	AGCAGCAAAG	GGGCTGACAC	GTGCCAGGGC	GATTCTGGAG	GCCGCCCTGGT	660
GTGTGATGGT	GCACTCCAGG	GCATCACATC	CTGGGGCTCA	GACCCTGTG	GGAGGTCCGA	720
CAAACCTGGC	GTCTATACCA	ACATCTGCCG	CTACCTGGAC	TGGATCAAGA	AGATCATAGG	780
CAGCAAGGGC	TGATTCTAG					799

(11) INFORMATION FOR SEQ ID NO: 10

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE:
 - (A) DESCRIPTION: protein
- (iii) HYPOTHETICAL: no
- (iv) ANTISENSE: no
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (vii) IMMEDIATE SOURCE:
- (viii) POSITION IN GENOME:
- (ix) FEATURE:
- (x) PUBLICATION INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ

Met Gly Arg Pro Pro Pro Cys Ala Ile Gln Pro Trp Ile Leu Leu
5 10 15

Leu Leu Phe Met Gly Ala Trp Ala Gly Leu Thr Arg Ala Gln Gly
20 25 30

Ser Lys Ile Leu Glu Gly Arg Glu Cys Ile Pro His Ser Gln Pro
35 40 45

Trp Gln Ala Ala Leu Phe Gln Gly Glu Arg Leu Ile Cys Gly Gly
50 55 60

Val Leu Val Gly Asp Arg Trp Val Leu Thr Ala Ala His Cys Lys
65 70 75

Lys Gln Lys Tyr Ser Val Arg Leu Gly Asp His Ser Leu Gln Ser
80 85 90

Arg Asp Gln Pro Glu Gln Glu Ile Gln Val Ala Gln Ser Ile Gln
95 100 105

His Pro Cys Tyr Asn Asn Ser Asn Pro Glu Asp His Ser His Asp
110 115 120

Ile Met Leu Ile Arg Leu Gln Asn Ser Ala Asn Leu Gly Asp Lys
125 130 135

Val Lys Pro Val Gln Leu Ala Asn Leu Cys Pro Lys Val Gly Gln
140 145 150

Lys Cys Ile Ile Ser Gly Trp Gly Thr Val Thr Ser Pro Gln Glu
155 160 165

Asn Phe Pro Asn Thr Leu Asn Cys Ala Glu Val Lys Ile Tyr Ser
170 175 180

Gln Asn Lys Cys Glu Arg Ala Tyr Pro Gly Lys Ile Thr Glu Gly
185 190 195

Met Val Cys Ala Gly Ser Ser Asn Gly Ala Asp Thr Cys Gln Gly
200 205 210

Asp Ser Gly Gly Pro Leu Val Cys Asp Gly Met Leu Gln Gly Ile
215 220 225

Thr Ser Trp Gly Ser Asp Pro Cys Gly Lys Pro Glu Lys Pro Gly
230 235 240

Val Tyr Thr Lys Ile Cys Arg Tyr Thr Thr Trp Ile Lys Lys Thr
245 250 255

Met Asp Asn Arg Asp
260